their regulatory functions in stages from the blastula to early neurula remain largely unknown. In our present study, we systematically knocked down the B1 *sox* genes in zebrafish. Only the quadruple knockdown of the four B1*sox* genes *sox2/3/19a/19b* resulted in very severe developmental abnormalities, confirming that the B1*sox* genes are functionally redundant. Phenotypic analyses of the *sox2/3/19a/19b* quadruple knockdown embryos revealed that the B1 SOX proteins regulate the following distinct processes: (1) early dorsoventral patterning by controlling *bmp2b/7*; (2) gastrulation movements via the regulation of *pcdh18a/18b* and *wnt11*, a non-canonical Wnt ligand gene; (3) neural differentiation by regulating the *Hes*-class bHLH gene *her3* and the proneural-class bHLH genes *neurog1* (positively) and *ascl1a* (negatively), and regional transcription factor genes, e.g., *hesx1*, *zic1* and *rx3*; and (4) neural patterning by regulating signaling pathway genes, *cyp26a1* in RA signaling, *oep* in Nodal signaling, *shh*, and *mdkb*. Chromatin immunoprecipitation analysis of the *her3*, *hesx1*, *neurog1*, *pcdh18a* and *cyp26a1* genes further suggests a direct regulation of these genes by B1 SOX. These findings indicate that the B1 SOX proteins control a wide range of developmental regulators in the early embryo and suggest that the B1*sox* functions are central to coordinating cell fate specification with patterning and morphogenetic processes occurring in the early embryo.

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Program/Abstract # 267
Role of the dlx cis-regulatory elements I56i and I56ii in zebrafish GABAergic interneuron development
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The *Dlx* homeobox genes play a role in the differentiation, migration and survival of subpallial precursor cells that mainly give rise to GABAergic interneurons. They also regulate the *Gad* genes encoding the enzymes necessary for GABA synthesis. In mice, at least four *cis*-acting regulatory elements (CREs) control *Dlx* expression in the telencephalon and diencephalon: I12b and URE2 in the *Dlx1/2* bigene cluster; I56i and I56ii in the *Dlx5/6* cluster. We showed that I56i marks GABAergic progenitors in the ganglionic eminences and subtypes of GABAergic cortical interneurons in adult mice. Activity of I56ii is found in a subpopulation of GABAergic striatal projection neurons at E11.5-E13.5. To investigate whether similar *Dlx*-mediated pathways exist in zebrafish, we established lines of transgenic zebrafish with reporter constructs containing a 1.4kb *Dlx5a/6a* intergenic fragment (encompassing I56i and I56ii) or a 295 bp fragment of I56i. Preliminary data revealed that EGFP-positive cells in the two lines largely overlap, at least in some domains of the telencephalon. Co-expression of EGFP with various GABAergic interneuron markers was observed in cells of the telencephalon and diencephalon starting at 2 dpf. We are examining whether morpholino knockdown of the *dlx* genes causes reductions in CRE activity and interferes with GABAergic neuron development. These studies will help us better understand the functional involvement of the *dlx* genes in an evolutionarily conserved pathway controlling GABAergic interneuron differentiation. Supported by CIHR, NSERC, and the Department of Cellular and Molecular Medicine, University of Ottawa.

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Program/Abstract # 268
Swi/Snf chromatin remodeling complexes control zebrafish neural patterning and differentiation
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In eukaryotic nuclei Swi/Snf chromatin remodeling complexes control nucleosome occupancy, balancing the necessity of DNA packaging with that of access to DNA by regulatory factors. Swi/Snf targeting is controlled by subunit make up, which is regulated by cell type and differentiation state. Swi/Snf complexes broadly belong either to the BAF or PBAF families. PBAF complexes are distinguished by the inclusion of specific subunits, such as Arid2. Using a morpholino targeting the zebrafish *arid2* gene, we have investigated Arid2 mediated PBAF function during development. Neural tissues are particularly sensitive to Arid2 depletion. *arid2* morphants lack specific neuronal and sensory cell populations and have posteriorization of the anterior neural plate. While the signals responsible for neural plate anteriorization appear normal in the absence of Arid2, expression domains of markers of forebrain and midbrain identities are reduced at the end of gastrulation. The reduction in anterior neural fates contrasts with hindbrain and spinal regionalizations, which are anteriorly shifted but otherwise normal. Therefore, anteriorizing signals are either not received or improperly transduced in *arid2* morphants. In order to identify potential Arid2 transcriptional targets responsible for anterior neural fates we are using ChIP-Seq techniques. Our findings demonstrate that we can successfully identify cell type and developmental stage specific roles for Swi/Snf chromatin remodeling complexes using whole animal targeting of specific Swi/Snf subunits.

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Program/Abstract # 269
Fox1 and Fox4 regulate muscle-specific splicing in zebrafish and are required for cardiac and skeletal muscle functions
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Fox RNA binding proteins are important regulators of tissue-specific splicing in vertebrates. Using human exon array and zebrafish bioinformatic data, we have identified and validated numerous muscle-enriched exons with conserved Fox binding motifs in adjacent introns. We tested the function of Fox proteins using antisense-mediated knockdown in zebrafish embryos. Depletion of two muscle-enriched fox paralogs, Fox1 and Fox4, results in significant changes in splicing of 12 predicted target exons and uncovers both distinct and redundant roles for Fox1 and Fox4 in the regulation of alternative splicing. Furthermore, combined Fox1/Fox4 depletion induces specific and dramatic morphological defects. Despite a relatively normal overall appearance, Fox1/Fox4-depleted embryos exhibit ventricular hypotrophy, reduced heartbeat, and blood circulatory defects. Additionally, depleted embryos are nearly completely paralyzed, indicating that Fox proteins regulate genes that have a role in muscle contraction and/or motor neuron function rather than in skeletal muscle specification. Importantly, Fox-depleted embryos co-injected with fox mRNAs rescue splicing of predicted Fox-regulated exons and the cardiac, blood, and motility defects. Our findings indicate that Fox proteins are important regulators of muscle-specific splicing